Amendments to the Specification:

Additions are indicated by underlining and deletions are indicated by ~~strikethrough~~.

A. Please replace the paragraph at page 80, lines 1-14, with the following amended paragraph:

A library of sequences of framework regions of human Ig heavy chain variable domains is then prepared for diversification, e.g, recombination or recursive recombination, as follows: Using the Kabat numbering system, each murine Ig heavy chain variable domain framework amino acid sequence and murine Ig CDR amino acid sequence is aligned (e.g., by aligning electronically or manually) with all or a portion (subset) of the human heavy chain variable domain framework amino acid sequences and CDR amino acid sequences included in the Kabat database using the SeqhuntII program's Match function ~~(http://immuno.bme.nwu.edu/scripts/websearch.tcl)~~ or an equivalent alignment program. In some cases, it is desirable to elect a predetermined number of mismatches to insure that the final recombinant heavy chain framework region possesses a desired degree of similarity to the donor heavy chain framework amino acid sequence. For example, if the number of mismatches is chosen to be greater than or equal 0.35 x the number of residues in a given framework, then the resulting recombinant heavy chain framework amino acid sequence is less than 65% identical to the donor heavy chain framework amino acid sequence.

B. Please replace the paragraph at page 91, line 14 to page 92, line 2 with the following amended paragraph:

BLAST is described in Altschul *et al., J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N= -4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).